Amendments to the Specification:

Please insert the following paragraph after paragraph [0001], and renumber paragraphs accordingly:

SEQUENCE LISTING

This application contains a "lengthy" Sequence Listing that has been submitted via triplicate CD-R in lieu of a printed paper copy, and is hereby incorporated by reference in its entirety. The CD-Rs, are labeled "CRF," "Copy 1" and "Copy 2," respectively. Each was recorded on November 17, 2003 and contains only one identical 790KB file named 34536321.APP.

Please substitute the following paragraph for the paragraph bridging pages 11-12 of the specification (currently paragraph 0041):

[0001] Several other proteins contain protein kinase-like homology including: receptor guanylyl cyclases, diacylglycerol kinases, choline/ethanolamine kinases, and YLK1-related antibiotic resistance kinases. Each of these families contain short motifs that were recognized by our profile searches with low scoring E-values, but a *priori* would not be expected to function as protein kinases. Instead, the similarity could simply reflect the modular nature of protein evolution and the primal role of ATP binding in diverse phosphotransfer enzymes. However, two recent papers on a bacterial homologue of the YLK1 family suggests that the aminoglycoside phosphotransferases (APHs) are structurally and functionally related to protein kinases. There are over 40 APHs identified from bacteria that are resistant to aminoglycosides such as kanamycin, gentamycin, or amikacin. The crystal structure of one well characterized APH reveals that it shares greater than 40% structural identity with the 2 lobed structure of the catalytic domain of cAMP-dependent protein kinase (PKA), including an N-terminal lobe composed of a 5-stranded antiparallel beta sheet and the core of the C-terminal lobe including several invariant segments found in all protein kinases. APHs lack the GxGxxG normally present in the loop between beta strands 1 and 2 but contain 7 of the 12 strictly

conserved residues present in most protein kinases, including the HGDxxxN (SEQ ID NO: 137) signature sequence in kinase subdomain VIB. Furthermore, APH also has been shown to exhibit protein-serine/threonine kinase activity, suggesting that other YLK-related molecules may indeed be functional protein kinases.

Please substitute the following paragraph for the second paragraph on page 37 (currently paragraph 0129):

[0129] In one embodiment, the polypeptide comprises a fusion protein which includes a heterologous region used to facilitate purification of the polypeptide. Many of the available peptides used for such a function allow selective binding of the fusion protein to a binding partner. A preferred binding partner includes one or more of the IgG binding domains of protein A are easily purified to homogeneity by affinity chromatography on, for example, IgG-coupled Sepharose. Alternatively, many vectors have the advantage of carrying a stretch of histidine residues that can be expressed at the N-terminal or C-terminal end of the target protein, and thus the protein of interest can be recovered by metal chelation chromatography. A nucleotide sequence encoding a recognition site for a proteolytic enzyme such as enterokinase, factor X procollagenase or thrombine may immediately precede the sequence for a kinase polypeptide to permit cleavage of the fusion protein to obtain the mature kinase polypeptide. Additional examples of fusion-protein binding partners include, but are not limited to, the yeast I-factor, the honeybee melatin leader in sf9 insect cells, 6-His tag (SEQ ID NO: 138), thioredoxin tag, hemaglutinin tag, GST tag, and OmpA signal sequence tag. As will be understood by one of skill in the art, the binding partner which recognizes and binds to the peptide may be any ion, molecule or compound including metal ions (*e.g.*, metal affinity columns), antibodies, or fragments thereof, and any protein or peptide which binds the peptide, such as the FLAG tag.

Please substitute the following paragraph for the second full paragraph on page 115 (currently paragraph 0394):

[0394] CRIK, SEQ ID NO: 1, SEQ ID NO: 67, is a member of the Protein Kinase superfamily. It is further classified into the AGC group, and the DMPK family. The nucleic acid sequence is 8656 nucleotides long, and codes for a protein that is 2055 amino acids long. The open reading frame starts at nucleotide number 51 and ends at nucleotide number 6218. The length of the ORF is 6168 nucleotides. The full length cDNA for this gene has been cloned. The gene has been mapped to chromosomal region 12q24.31. The CRIK sequence maps to Celera contig 181000000794572. A mouse homolog (Rho/rac interacting citron kinase gi|3599509) of CRIK is 353 AAs longer at the N terminus than the public CRIK. Rho/rac interacting citron kinase from mouse (gi|3599509) was used as a model for a genewise prediction. Incyte template, 233643.1, and Incyte CB1 sequence, 7484498CB1, were used to extend the C-terminus of the genewise prediction. Two additional public ESTs (gi|4534019 and gi|3753446) support a different 3' end. These two public ESTs (gi|4534019 and gi|3753446) have an earlier polyA site, just after ATTCTTAATAGATTTGAATAGCGACGTA **(SEQ ID NO: 139)** (just following the run of T's), this generates an alternative 3' end in that form.

Please substitute the following paragraph for the second full paragraph on page 121 (currently paragraph 0419):

[0419] ERK7, SEQ ID NO: 21, SEQ ID NO: 87, is a member of the Protein Kinase superfamily. It is further classified into the CMGC group, and the MAPK family. The nucleic acid sequence is 1906 nucleotides long, and codes for a protein that is 563 amino acids long. The open reading frame starts at nucleotide number 19 and ends at nucleotide number 1710. The length of the ORF is 1692 nucleotides. The full length cDNA for this gene has been cloned. The gene has been mapped to chromosomal region 8q24.3. A genewise prediction was run with a rat homolog, extracellular signal-regulated kinase 7 (gi|4220888), as the model. Two splice variants were noted for ERK7:
>Nucleotides 967 – 1098 **of SEQ ID NO: 21** are alternatively spliced
GCACTGCAGCACCCCTACGTGCAGAGGTTCCACTGCCCCAGCGACGAGTGGGCACGAGA
GGCAGATGTGCGGCCCCGGGCACACGAAGGGGTCCAGCTCTCTGTGCCTGAGTACCGCA

GCCGCGTCTATCAG. >Nucleotides 184 – 240 **of SEQ ID NO: 21** are alternatively spliced GACATGGGCTTCCTTCTTGCTCCACCCACCCACACACCTGTGTTTCTGTCTCTTCAG.

Please substitute the following paragraph for the second full paragraph on page 124 (currently paragraph 0430):

[0430] The revised sequence now contains a complete kinase domain and overlaps completely with the mouse ortholog of Nek1 (gi|1709251). Three alternative splice variants were noted: >Nucleotides 243 – 320 **of SEQ ID NO: 29** (canonical splice sites maintained) gtgtggagagtctcagtgccccctttcagtctggactgtgagctgctgctggttagacagtcttggtttctctttcag. >Nucleotides 1923 – 2054 **of SEQ ID NO: 29** (canonical splice sites maintained) AGGAATTCTGCCTGGAGTTCGTCCAGGATTTCCTTATGGGGCTGCAGGTCATCACCATTT TCCTGATGCTGATGATATTAGAAAAACTTTGAAAAGATTGAAGGCGGTGTCTAAACAAG CCAATGCAAACAG. >Nucleotides 2158 – 2241 **of SEQ ID NO: 29** (canonical splice sites maintained).
GGAATCCTGCAAAACCTGGCAGCTATGTATGGAGGCAGGCCCAGCTCTTCAAGAGGAGG GAAGCCAAGAAACAAAGAGGAAGAG.

Please substitute the following paragraph for the paragraph bridging pages 125-126 (currently paragraph 0437):

[0437] >Nucleotides (insert after nucleotide 1697) **SEQ ID NO: 133**
GTGAGGCGCTCAGGTGGACACTGTTCCCCTGACTCACCCCCACCCTAGCAGCTGAGGGA AGCCGGGGATAAAAGAGGCTGCTGAAGCATCCAGCCTCGTGGTGGCCTAATTGGCTGTG TGTCACCAGCCTGGCGGGGCTGACCTGGGGTGCCCTGGGAGCCAGGGCAGGGCCAGGCC ATGGACTCAAGGGTTTGGATTTTGGGGCCTGTGTCACTCCCTTTCCCTGCCCAACCCTCC AG
>Nucleotides 2039 –2168 **of SEQ ID NO: 34**

GACTGTGCACTACAATCCCACCAGCACAAAGCACTTCTCCTTCTCCGTGGGTGCTGTGCC
CCGGGCCCTGCAGCCTCAGCTGGGTATCCTGCGGTACTTCGCCTCCTACATGGAGCAGCA
CCTCATGAAG

Please substitute the following paragraph for the first paragraph on page 127 (currently paragraph 0441):

[0441] One alternative splice variant was noted:
>Nucleotides 645 – 707 **of SEQ ID NO: 37**
GTTCCCCAACCTCCCGGTCTTCCAGTCCTTGGCCTATTGGGAAATGGGTCGTACAGCAGG
AGG.

Please substitute the following paragraph for the paragraph bridging pages 128-129 (currently paragraph 0447):

[0447] Six alternative splice variants are noted:

> Wnk2, SEQ ID NO: 42 Nucleotides 2059 ~~and~~ - 2214
CCTGGCTTGCCGGTGGGCTCTGTCCCGGCCCCCGCCTGCCCTCCGTCCCTCCAGCAGCAC
TTCCCGGATCCGGCCATGAGCTTCGCCCCCGTGCTGCCGCCGCCCAGCACCCCCATGCCC
ACGGGCCCAGGCCAGCCAGCACCCCCCGGCCAGCAG

>Wnk2, SEQ ID NO: 42 Nucleotides 5945 ~~and~~ - 6136
GTCACTTGGCTGACTCCAGCAGAGGCCCTCCCGCTAAGGACCCTGCCCAAGCCAGTGTGG
GGCTCACTGCAGACAGCACGGGCCTGAGCGGGAAGGCAGTGCAGACCCAGCAGCCCTGC
TCCGTCCGGGCCTCCCTGTCTTCGGACATCTGCTCCGGCTTAGCCAGTGATGGAGGCGGA
GCGCGTGGCCAAG

> Wnk2, SEQ ID NO: 42Nucleotides 6137 **and** - 6280

GCTGGACGGTTTACCACCCAACGTCTGAGAGAGTGACCTATAAGTCTAGTAGCAAACCT
CGTGCTCGATTCCTCAGTGGACCCGTATCTGTGTCCATCTGGTCTGCCCTGAAGCGTCTCT
GCCTAGGCAAAGAACACAGCAGTA

> Wnk2, SEQ ID NO: 42 Nucleotides 5945 ~~and~~ - 6280
GTCACTTGGCTGACTCCAGCAGAGGCCCTCCCGCTAAGGACCCTGCCCAAGCCAGTGTGG
GGCTCACTGCAGACAGCACGGGCCTGAGCGGGAAGGCAGTGCAGACCCAGCAGCCCTGC
TCCGTCCGGGCCTCCCTGTCTTCGGACATCTGCTCCGGCTTAGCCAGTGATGGAGGCGGA
GCGCGTGGCCAAGGCTGGACGGTTTACCACCCAACGTCTGAGAGAGTGACCTATAAGTC
TAGTAGCAAACCTCGTGCTCGATTCCTCAGTGGACCCGTATCTGTGTCCATCTGGTCTGC
CCTGAAGCGTCTCTGCCTAGGCAAAGAACACAGCAGTA

> Wnk2, SEQ ID NO: 42 Insert after nucleotide 620, **SEQ ID NO: 134**
TCTGTGCGGTTGACTCCTTTTCCTCCCCGCCTGGAGATCCCCGTGGTGTCGACTGGAAGC
ATGGAGGCACCTTGGGGAG

> Wnk2, SEQ ID NO: 42 Replaces nucleotides 6650 – 7981, **SEQ ID NO: 135**
ATCCTGAGAGTGAGAAGCCTGACTGACCCCGCCTAGACGCCAGGCCCACTTCACGCCGT
CTAAGTGGAGAAGTGACGGACCCTCAGGGCCAGCTGCTCCTCCTGTCCAGTTCACGCTGT
TTTGTAACCACTTTCTAAGCATTTTTTATTCACAATTGGAAACACAAATGTAATGCAAGA
ATAAAAAATATTTTGGGGCAGAAAGGACTTTGGTTTTTCAAACTATTTCCTCTCTGGTGG
CCCTCGGCCAGCCAGGTGACTGGGATGTGACAGGGGTGGGGGGACATTCCCAGGACCCT
GGCATGCTCAGGATAGCCCTGTTCTCTGCAGGGCCCTGGAGGTGGCGGCCCCGGGGAGG
CTGATCTCCAAGTCCCCCCGATGCCAGCTGGC

Please substitute the following paragraph for the second paragraph on page 130 (currently paragraph 0451):

[0451] One alternative splice variant was noted:
>MAP3K8, SEQ ID NO: 44 Replaces nucleotides 1412 – 2571, **SEQ ID NO: 136**
GTTCAAGTCCAATGGGAAAGAAATATCTTCCTTCAACAGCTGAATATGTTACTGGAAGTT
TGGAGAATCATTACTAGATGGCAAAAACAAAAGATGTTCCTTCCATTTTGTGAACTGCAT

AAGAGATCTTGGGGGGTGGGCGATGAAGAGAGGTATACTGTGGTCTCACTAGTCAAGGA
CAGCTAATAGCTGTAAAACAGGTGGCTTTGGATAACT

Please substitute the following paragraph for the paragraph bridging pages 206-207 (currently paragraph 0735):

[0735] The most common variations in human DNA are single nucleotide polymorphisms (SNPs), which occur approximately once every 100 to 300 bases. Because SNPs are expected to facilitate large-scale association genetics studies, there has recently been great interest in SNP discovery and detection. Candidate SNPs for the genes in this patent were identified by blastn searching the nucleic acid sequences against the public database of sequences containing documented SNPs (dbSNP: sequence files were downloaded from ftp: //ncbi.nlm.nih.gov/SNP/human/rs-fasta/ and ftp: //ncbi.nlm.nih.gov/SNP/human/ss-fasta/ and used to create a blast database). dbSNP accession numbers for the SNP-containing sequences are given. SNPs were also identified by comparing several databases of expressed genes (dbEST, NRNA) and genomic sequence (i.e., NRNA) for single base pair mismatches. The results are shown in Table 3. These are candidate SNPs – their actual frequency in the human population was not determined. The code below is standard for representing DNA sequence:

G = Guanosine
A = Adenosine
T = Thymidine
C = Cytidine
R = G or A, puRine
Y = C or T, pYrimidine
K = G or T, Keto
W = A or T, Weak (2 H-bonds)
S = C or G, Strong (3 H-bonds)
M = A or C, aMino
B = C, G or T (i.e., not A)
D = A, G or T (i.e., not C)
H = A, C or T (i.e., not G)

V = A, C or G (i.e., not T)

N = A, C, G or T, aNy

X = A, C, G or T

complementary G A T C R Y W S K M B V D H N X **(SEQ ID NO: 140)**

DNA +-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+

strands C T A G Y R S W M K V B H D N X **(SEQ ID NO: 141)**

Please substitute the following paragraph for the paragraph bridging pages 250-251 (currently paragraph 0936):

[0936] Individual plaques are picked into 25 μL of 10 mM EDTA and the phage is disrupted by heating at 70 °C for 10 min. 2 μL of the disrupted phage are added to 50 μL PCR reaction mix. The insert DNA is amplified by 35 rounds of thermal cycling (94 °C, 50 sec; 50 °C, 1min; 72 °C, 1min).

Composition of Buffer

10x PanMix

5% Triton X-100

10% non-fat dry milk (Carnation)

10 mM EGTA

250 mM NaF

250 μg/mL Heparin (sigma)

250 μg/mL sheared, boiled salmon sperm DNA (sigma)

0.05% Na azide

Prepared in PBS

Wash Buffer

PBS supplemented with:

0.5% NP-40

25 μl g/mL heparin

PCR reaction mix

1.0 mL 10x PCR buffer (Perkin-Elmer, with 15 mM Mg)

0.2 mL each dNTPs (10 mM stock)

0.1 mL T7UP primer (15 pmol/μL) GGAGCTGTCGTATTCCAGTC

(SEQ ID NO: 142)

0.1 mL T7DN primer (15 pmol/μL) AACCCCTCAAGACCCGTTTAG

(SEQ ID NO: 143)

0.2 mL 25 mM $MgCl_2$ or $MgSO_4$ to compensate for EDTA

Q.S. to 10 mL with distilled water

Add 1 unit of Taq polymerase per 50 μL reaction

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